

ID Q9V718 PRELIMINARY; PRT; 987 AA.
AC Q9V718;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG8414 PROTEIN.
GN CG8414.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE; 20196006.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003808; AAF58067.1; -.
DR FLYBASE; FBgn0034073; CG8414.
DR SEQUENCE 987 AA; 110425 MW; E10CD3B7B10BCAA CRC64;

Query Match 11.3%; Score 91; DB 5; Length 987;
Best Local Similarity 31.5%; Pred. No. 2.7;
Matches 35; Conservative 21; Mismatches 47; Indels 8; Gaps 5;

QY 24 KRQP-VFEDMTDIDQASAPQRLIYKDKSEVGLAVTLVSKSKXSTLSCKNKTIISF 82
Db 373 QREPLIEIFD-DPVEKKQRIEQSSVMDIVKNLSVPPKKESEVAIETEENDEVS 431
QY 83 EEMDPENIDDIQ-SDLIFQKRVGNHME--FESSLYEGHFLACQKED 129
Db 432 PEVVTPEKENYLPQSDVPFY--RNQANPTELSVFENSLKSNHVLAVIKED 480

RESULT 3
Q9Y1J4

ID Q9Y1J4 PRELIMINARY; PRT; 784 AA.
AC Q9Y1J4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RETINOID X RECEPTOR RXR-2.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE; 99307140.
RA Freebern W.J., Niles E.G., Loverde P.T.;
RT "RXR-2, a member of the retinoid x receptor family in Schistosoma
mansoni.";
RL Gene 233:33-38(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF129816; AAD33428.1; -.
DR INTERPRO; IPR000324; -.
DR INTERPRO; IPR000536; -.
DR INTERPRO; IPR001628; -.
DR PFAM; PF00104; hormone_rec; 1.
DR PFAM; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00350; VITAMINDR.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
SQ SEQUENCE 784 AA; 87249 MW; CD35E449E5FD547F CRC64;

Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;

QY 46 LIIVMYKDSVVRGLAVTLVSKSKXSTLSCKNKTIISFEMDPEN-IDDIQSDLI----- 100
Db 513 LVVYWLANDHKPRSLSTNSSTSKLPDPTPTINSTDISNTDDPPENSISDISKPTIQMK 572
QY 101 FQKRVGNHME-FESSLYEGHFLACQKEDDAFLIKKKDENGDKSVMTLTNLHQS 157
Db 573 INKSVPLDEKMDYYSNFPERHLL-----NNLTKPMDDNNNDSSISKPTININDN 621

RESULT 4
Q9U9R6 PRELIMINARY; PRT; 784 AA.
AC Q9U9R6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE RETINOID-X-RECEPTOR.
GN RXR.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RA Mendonca R.L., Escrivá H., Bouton D., Vanacker J.-M., Zelus D.,
RA Bonnelly E., Pierce R., Laudet V.;
RT "A Schistosoma mansoni nuclear receptor of the RXR family shows marked
structural and functional divergence from vertebrate and arthropod
homologs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF158102; AAD45325.1; -.
DR INTERPRO; IPR000324; -.
DR INTERPRO; IPR000536; -.
DR INTERPRO; IPR001628; -.
DR INTERPRO; IPR001723; -.
DR PFAM; PF00104; hormone_rec; 1.
DR PFAM; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.

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DR PRINTS; PR00350; VITAMINDR.
DR PRINTS; PR00398; STRDHOMONER.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 784 AA; 87250 MW; 471DAE69EB135A9F CRC64;

Query Match	10.68;	Score 85.5;	DB 5;	Length 784;
Best Local Similarity	27.18;	Pred. No. 6.6;		
Matches 32; Conservative	18;	Mismatches 53;	Indels 15;	Gaps 4;

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QY      46 LIIMYKDESVRGLAVITSVKDKSKXSLSCKNKITSFEEMDPEN-IDDIQSLIF----- 100
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      513 LVYWLANDHHRPSRLSTSNSTSKLPDTPPTINSTDINSITDDPENSISDISKCTIOMKK 5722
QY      101 FQKRVPVGHNKE-FESSLYEGHFLACOKEDDAFKLILKKKDENGDSVMFTTLNLHOS 157
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      573 INKSVPLDEKMDYYISNPEEFHL-----NNLTKPMDNNDNISISKPTINDN 621
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RESULT	5
Q9UA14	
ID	Q9UA14
PRELIMINARY;	
PRT;	482 AA

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ne 01-MAY-2000 (TREMBlrel. 13, Created)
dt 01-MAY-2000 (TREMBlrel. 13, last sequence update)
dt 01-JUN-2000 (TREMBlrel. 14, last annotation update)
DE PROTEIN PHOSPHATASE 2A 55 KDA REGULATORY B SUBUNIT (FRAGMENT).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 99379588.
RX Murphy M.B., Levi S.K., Egelhoff T.T.;
RA "Molecular characterization and immunolocalization of Dictyostelium
RT discoideum protein phosphatase 2A.";
RL FEBS Lett. 456:7-12(1999).
DR EMBL; AF138279; AAD29694.1; -.
DR INTERPRO; IPR000009; -.
DR INTERPRO; IPR001680; -.
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; PP2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
FT NON_TER 1 1
SQ SEQUENCE 482 AA; 55107 MW; 95E879E7A37D2392 CRC64;

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Query Match	10.58;	Score 85;	DB 5;	Length 482;
Best Local Similarity	25.98;	Pred. No. 4.2;		
Matches 36;	Conservative 23;	Mismatches 58;	Indels 22;	Gaps 6

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OY      14 NINDOVL-EVDKROPVFEDMTDIDOSASEPQTRLIYYMKDSEVRLAVTLVSXKDSKXT 72
        ||| : || : ||| :: | | :||| | : : : |
Db      236 NINTECFNVADIKPTNMEDELTEVITSAEHPHTSCNIFWYSSSK-----GTIKGLDRSSA 290
OY      73 LSCKNKIISFEEMDPENIDDIQSDLIFPQKRVPGNHNMKEFESSLSLEGHFLACQKEDDAF 132
        | | | ||| : | | | : : : : : : : :
Db      291 L-CDNHAKVFEELEDPSNKS-----PFSELISLSDIKFSR---DGRYLIRD----- 334
OY      133 KLILKKKDENGDKSVMEFTL 151
        | | | | : : : : : : : :
Db      335 FLTLKLMDINMENKPKVTI 353
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RESULT	6	
Q9Y0A6		
ID	Q9Y0A6	PRELIMINARY;
AC	Q9Y0A6;	PRT; 483 AA.
DT	01-NOV-1999	(TREMBLrel. 12, Created)
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)

DE PROTEIN PHOSPHATASE 2A B5 REGULATORY SUBUNIT.
GN PPPD.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Campanha R.B., Etchebehere L.C., da Silva A.M.;
RT "Functional analysis of a B regulatory subunit of protein phosphatase
RT 2A in D. discoideum.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167979; AAD45396.1; -.
DR INTERPRO: IPR000009; -.
DR INTERPRO: IPR001680; -.
DR PFAM; PF01240; PR55_1.
DR PRINTS; PR00600; PP2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
SQ SEQUENCE 483 AA; 55275 MW; DCF9434FE95C27BE CRC64;

Query Match	10.5%;	Score 85;	DB 5;	Length 483;
Best Local Similarity	25.9%;	Pred. No. 4.2;		
Matches	36;	Conservative	23;	Mismatches
			58;	Indels
				22;
				Gaps
				6;

[illegible]

RESULT	7	
073909		
ID	073909	PRELIMINARY; PRT; 267 AA

DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	INTERLEUKIN-1BETA.
GN	IL-1BETA.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Weining R.C., Sick C., Kaspers B., Staeheli P.;
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; Y15006; CAA75239.1; -.
DR	HSSP; P18510; 1IRA.
DR	INTERPRO: IPR000975; -.
DR	PRAM; PF00340; interleukin-1; 1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
FT	CHAIN 106 INTERLEUKIN-1BETA.
SQ	SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;

Query Match	10.38;	Score 83;	DB 13;	Length 267;
Best Local Similarity	24.88;	Pred. No. 3.2;		
Matches	30;	Conservative	18;	Mismatches 45;
				Indels 28;
				Gaps 4

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QY      31 DMTDIDQS-----ASEPQRLIIMYKDESEVRGLA-----VTLSVK 66
      1 : ||:| : : : | | : | : |
Db     118 DIFDINQCFVLESPQLVALHLQGPSSSKVRNLNIALYRPRGPGSAGTGQMPVALGIK 177

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QY 67 DSK--XSTLSCNKKIISFEEMDPENIDDIQ-SDLIFQKRVGHNKMEFESSLYEGHF 122
 DB 178 GYKLYMSCVMSGTEPTLQLEADVMDIDSVELTRFIYFLDSEPTGTRFESAAPGWF 237
 QY 123 L 123
 DB 238 I 238

RESULT 8

Q9XV67 PRELIMINARY; PRT; 483 AA.
 AC Q9XV67;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE F25C8.2 PROTEIN.
 GN F25C8.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA Matthews L.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
 RL Nature 368:32-38(1994).
 DR EMBL; Z81512; CAB04171.1; -.
 DR INTERPRO; IPR002937; -.
 DR PFAM; PF01593; Amino_oxidase; 1.
 SQ SEQUENCE 483 AA; 55505 MW; 172CEC91495557AB CRC64;

Query Match 10.0%; Score 81; DB 5; Length 483;
 Best Local Similarity 26.4%; Pred. No. 9.8;
 Matches 55; Conservative 24; Mismatches 63; Indels 66; Gaps 12;

QY 3 GRHCTTAVIRNINDV-----LFVDRKQPYEEDMTDIDQAS-----EPQTRLIT 48
 DB 81 GYLHFGAEYVNGVDNEVYNLVEKYDLF-DKTKPRTDLMMLDQDNSTLLVNGHLVPPKIL 139
 QY 49 YMKDSEVRGLAVTLVSKDSKXSTLSCNKKIIS-FEEM--DPENIDDIQSDLIFFQKRV 105
 DB 140 DKEND-YIRYLNVALYEKSTIKINQLSVENINNOQFTEFLRDVPENDHEIYESLINVYK-- 196
 QY 106 PGHNKMEFESSLYEGHFL-----ACQKEDDA-----FKLILK----- 137
 DB 197 ---NYQTEWSSPVGELSLNSLSIMWDDGTEEDSAVLNKQGFYEILKDFRSKIPAGNIRL 253
 QY 138 -----KKDENGDKSVAFTLTN---LH 155
 DB 254 NCEVINVKKEEN-----IMVTLKNGEVLH 277

RESULT 9
 Q29082

ID Q29082 PRELIMINARY; PRT; 267 AA.
 AC Q29082;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE INTERLEUKIN 1-BETA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Vanderbroeck K.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE; 94039070.
 RA Vandenbroeck K., Fiten P., Beuken E., Martens E., Janssen A., Van Damme J., Opdenakker G., Billiau A.;
 RT "Gene sequence, cDNA construction, expression in Escherichia coli and genetically approached purification of porcine interleukin-1 beta.";
 RT Eur. J. Biochem. 217:45-52(1993).
 RL EMBL; X74568; CAA52660.1; -.
 DR HSSP; P01584; IHTB.
 DR INTERPRO; IPR000975; -.
 DR INTERPRO; IPR002348; -.
 DR PFAM; PF00340; Interleukin-1; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRINTS; PR00264; INTERLEUKIN1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 SQ SEQUENCE 267 AA; 29893 MW; 4830645DA5FF9967 CRC64;

Query Match 10.0%; Score 80.5; DB 6; Length 267;
 Best Local Similarity 28.6%; Pred. No. 5.5;
 Matches 24; Conservative 22; Mismatches 25; Indels 13; Gaps 6;

QY 53 DSEVRGLAVTLVSKDSKXSTLSCNKKIISFEEMDP--PENIDDIQSDLIFFQKRV 105
 DB 165 DSDDK-IPVYLGK-GKNLYLSCVMDPTPTQLLEDVDPKSTPKR--DMKRFVYKTEI 220
 QY 106 PGHNKMEFESSLYEGHFLACQKED 129
 DB 221 --KNRVFEFSALYPNWIISTSQAE 242

RESULT 10
 Q24892 PRELIMINARY; PRT; 414 AA.
 AC Q24892;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CALMODULIN-DOMAIN PROTEIN KINASE (FRAGMENT).
 OS Eimeria maxima.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 OC Eimeria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOUGHTON;
 RX MEDLINE; 96089387.
 RA Bumstead J.M., Dunn P.P.J., Tomley F.M.;
 RT "Nitrocellulose immunoblotting for identification and molecular gene cloning of Eimeria maxima antigens that stimulate lymphocyte proliferation.";
 RT Clin. Diagn. Lab. Immunol. 2:524-530(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOUGHTON;
 RX MEDLINE; 97048698.
 RA Dunn P.P.J., Bumstead J.M., Tomley F.M.;
 RT "Sequence, expression and localization of calmodulin-domain protein

RT	kinases in Eimeria tenella and Eimeria maxima.";		
RL	Parasitology 113:439-448(1996).		
DR	EMBL; Z71756; CAA96438.1; -.		
DR	HSSP; Q63450; IA06.		
DR	INTERPRO; IPR000719; -.		
DR	INTERPRO; IPR002048; -.		
DR	INTERPRO; IPR002290; -.		
DR	PFAM; PF00036; ehand; 4.		
DR	PFAM; PF00069; pkinase; 1.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN4.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
FT	NON_TER	1	1
SQ	SEQUENCE	414 AA;	47427 MW; 7B0C793F0A45BA68 CRC64;

Query Match	10.0%;	Score 80.5;	DB 5;	Length 414;
Best Local Similarity	25.7%;	Pred. No. 9.1;		
Matches 29;	Conservative 21;	Mismatches 42;	Indels 21;	Gaps 4;
QY 42	PQTRLIIYWKDSEVRGLA----	VTLSVKDS-----	KXSTLSCKNKIISFEEMDP	PENI 91
	: : : : :	: : : :	: : : :	:
DB 174	PQWRKVSSEPAKDLIRKMLAYVP	PSMRISAKDALDHPWIKST	DVIYAKDSI-----	NL 223
QY 92	DDIOSDLFFQKRVPGHNKMEF	SESLSYEGHFLACQKEDDA	FKFLILKKDDE	NGD 144
	::: : : : :	: : : :	: : : :	: : : :
DB 224	PSLESTLINI-RQFOGTOKLAA	AAALYMGSKLTNEETDEL	NKTFQOMDKND	275

RESULT	11
084869	
ID	084869
AC	084869;
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT	01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE	HYPOTHETICAL 56.5 KDA PROTEIN.
GN	CT861.
OS	Chlamydia trachomatis.
OC	Bacteria; Chlamydiales; Chlamydiaeae; Chlamydia.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=D/UW-3/CX;
RX	MEDLINE: 99000809.
RA	Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA	Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA	Davis R.W.;
RT	"Genome sequence of an obligate intracellular pathogen of humans:
RT	Chlamydia trachomatis.";
RL	Science 282:754-759(1998).
DR	EMBL: AE001359; AAC68459.1; -.
KW	Hypothetical protein.
QO	SEQUENCE 506 AA; 56464 MW; 4FAA4A12C1098BB4 CRC64;

Query Match	9.9%	Score 80;	DB 2;	Length 506;
Best Local Similarity	25.0%;	Pred. NO. 13;		
Matches 38;	Conservative 25;	Mismatches 55;	Indels 34;	Gaps 7;
QY	1	NFGRHCTTAVIRNINDOVL	FVYDKQPVFEDMTDIDQASAEQTRLI	MYKDXSEVRGLA 60
	:			
Db	63	SFSRLQPTTP----	KERILFFGS-SPSSQLSIVRTTSSFWN----	LFSNSQTRNST 111
QY	61	VTLSVKDSKXSTLSCRN--	KLIISFEEMDPENIDDIQSDLI	FFQKRVPGHNKMEFESSLY 118
	:			
Db	112	RKLSERKLHFSSELSARDSTK	PSSSEPIKPESENTL-----	LHTPEHRK-ELFSSSLK 159
QY	119	EGHFLACOKEDDAF-----	KLILKKDE	141
	:			
Db	160	KDNLSPIMEEIDSFSAETESL	EERLVTQKKEE	191
	:			
RESULT	12			

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Q9YF27      Q9YF27      PRELIMINARY;      PRT; 1039 AA.
ID      Q9YF27
AC      Q9YF27;
DT      01-NOV-1999 (TrEMBLrel. 12, Created)
DT      01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT      01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE      HYPOTHETICAL 120.0 KDA PROTEIN APE0413.
GN      APE0413.
OS      Aeropyrum pernix.
OC      Archaea; Crenarchaeota; Desulfurococcaceae;
OC      Aeropyrum.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-K1;
RX      MEDLINE; 99310339.
RA      Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA      Jin-no K., Takahashi M., Sekine M., Baba S., Ankaei A., Kosugi H.,
RA      Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA      Takamaya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA      Yamazaki J., Kushiida N., Oguchi A., Aoki K., Kubota K., Nakamura Y.,
RA      Nomura N., Sako Y., Kikuchi H.;
RT      "Complete genome sequence of an aerobic hyper-thermophilic
RT      crenarchaeon, Aeropyrum pernix K1.";
RL      DNA Res. 6:83-101(1999).
DR      EMBL; AP000059; BAA79369.1; -.
DR      INTERPRO; IPR000330; -.
DR      INTERPRO; IPR001410; -.
DR      INTERPRO; IPR001650; -.
DR      PFAM; PF00176; SNE2_N; 1.
DR      PFAM; PF00271; helicase_C; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 1039 AA; 119959 MW; 30C9191854575F9D CRC64;

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Query Match          9.7%; Score 78.5; DB 1; Length 1039;
Best Local Similarity 26.4%; Pred. No. 40;
Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;

QY 31 DMDIDOSASEPQTRLIYM-----YKDSVYGLAVTLISVSKSXSTL 73
   | : : | : | | | | | | | | | | | | | | | | | | | |
DB 374 DIGEIDELDEEERFLAIYFDKLLDDMFREELKKAOKYAEDILGVKAV-----DSKVETL 428
   | : : | : | | | | | | | | | | | | | | | | | | | |

QY 74 SCNNKIISFEEMDPENIDDIQSDLIIFQKRVPGHNKMEFESSLYEGHFLACQKEDAFK 133
   | : : | : | | | | | | | | | | | | | | | | | | | |
DB 429 --KKILGLVLTPPEELPDEFKDLA-SQKAIVFTEFKDTAFYLYE-----K 471
   | : : | : | | | | | | | | | | | | | | | | | | | |

QY 134 LILKKKDENGDKSYMFTLTN 153
   | : : | : | | | : : | : | : | : | : | : | : | : |
DB 472 LRKWADEDFGDPGLRVFTS 491
   | : : | : | | | : : | : | : | : | : | : | : | : |

RESULT 13
Q9RF17 PRELIMINARY; PRT; 388 AA.
AC Q9RF17:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PROTEIN I/II V-REGION (FRAGMENT).
OS Streptococcus gordonii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
CC [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PA47;
RA Chatenay-Rivauday C., Yamodo I., Sciolti M.A., Troffer-Charlier N.,
RT Klein J.P., Ogier J.;
RT "TNFalpha release by monocytic THP-1 cells through cross-linking of
RT the extended V-region of the oral streptococcal protein I/II.";
RL J. Leukoc. Biol. 0:0-0(2000).
DR EMBL; AF192472; AAF20187.1; -.
FT NON_TER 1 388 388 1

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